

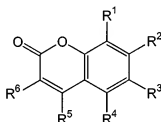
Amendments to the Claims:

This listing of claims will replace all prior versions, and listings of claims in the application:

Listing of Claims:

1-83 (canceled)

84 (previously presented): A material having a fluorogenic moiety linked to a solid support, said material having the structure:



wherein:

R¹, R³, R⁴ and R⁶ are each H;

R² is -NHR¹⁵; and

R⁵ is -R¹⁴-SS,

wherein:

R¹⁴ is -CH₂C(O)NH-;

R¹⁵ is a member selected from the group consisting of amine protecting groups, -C(O)-AA and -C(O)-P:

wherein:

P is a peptide sequence;

AA is an amino acid residue; and

SS is a solid support.

85 (previously presented): The material in accordance with claim 84, wherein R¹⁵ is an amine protecting group.

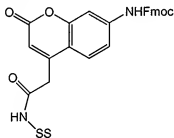
1 **86** (previously presented): The material in accordance with claim 85, wherein
2 said amine protecting group is 9-fluorenylmethoxycarbonyl (Fmoc).

1 **87** (previously presented): The material in accordance with claim 84, wherein
2 R¹⁵ is -C(O)-AA, wherein AA is an amino acid residue.

1 **88** (previously presented): The material in accordance with claim 84, wherein
2 R¹⁵ is -C(O)-P, wherein P is a peptide sequence.

1 **89** (previously presented): The material in accordance with claim 84, wherein
2 the solid support is a Rink resin.

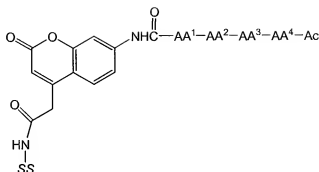
1 **90** (previously presented): A material having a fluorogenic moiety linked to a
2 solid support, said material having the structure:



3
4 wherein:

5 SS is a solid support, wherein said the support is a Rink resin.

1 **91** (withdrawn): A library of fluorogenic peptides comprising sub-libraries P1,
2 P2, P3 and P4, wherein each of the sub-libraries P1, P2, P3 and P4 comprises tetrapeptides
3 having the structure:



wherein:

SS is a solid support, and

wherein:

for sub-library P1, each AA¹ is a different amino acid of the 20 amino acids, and each of AA²-AA⁴ is an isokinetic mixture of 20 amino acids;

for sub-library P2, each of AA² is a different amino acid of the 20 amino acids, and each of AA¹, AA³ and AA⁴ is an isokinetic mixture of 20 amino acids;

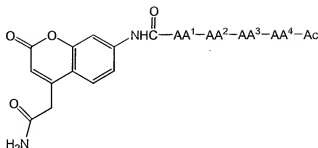
for sub-library P3, each of AA³ is a different amino acid of the 20 amino acids, and each of AA¹, AA² and AA⁴ is an isokinetic mixture of 20 amino acids; and

for sub-library P4, each of AA⁴ is a different amino acid of the 20 amino acids, and each of AA¹, AA² and AA³ is an isokinetic mixture of 20 amino acids.

92 (withdrawn): The library in accordance with claim 91, wherein the 20 amino acids are the 20 naturally occurring amino acids excluding cysteine and including norleucine.

93 (withdrawn): The library in accordance with claim 91, wherein the solid support is a Rink resin.

94 (withdrawn): A library of fluorogenic peptides comprising sub-libraries P1, P2, P3 and P4, wherein each of the sub-libraries P1, P2, P3 and P4 comprises tetrapeptides having the structure:



wherein:

for sub-library P1, each AA^1 is a different amino acid of the 20 amino acids, and each of AA^2-AA^4 is an isokinetic mixture of 20 amino acids;

for sub-library P2, each of AA^2 is a different amino acid of the 20 amino acids, and each of AA^1 , AA^3 and AA^4 is an isokinetic mixture of 20 amino acids;

for sub-library P3, each of AA^3 is a different amino acid of the 20 amino acids, and each of AA^1 , AA^2 and AA^4 is an isokinetic mixture of 20 amino acids; and

for sub-library P4, each of AA^4 is a different amino acid of the 20 amino acids, and each of AA^1 , AA^2 and AA^3 is an isokinetic mixture of 20 amino acids.

95 (withdrawn): The library in accordance with claim 94, wherein the 20 amino acids are the 20 naturally occurring amino acids excluding cysteine and including norleucine.

96 (withdrawn): A method of determining a peptide sequence specificity profile of an enzymatically active protease, said method comprising:

(a) contacting said protease with a library of peptides according to claim 91 or claim 94 in such a manner whereby the fluorogenic moiety is released from the peptide sequence, thereby forming a fluorescent moiety;

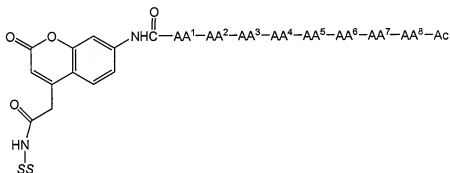
(b) detecting said fluorescent moiety;

(c) determining the sequence of said peptide sequence, thereby determining said peptide sequence specificity profile of said protease.

97 (withdrawn): The method according to claim 96, further comprising (d) quantifying said fluorescent moiety, thereby quantifying said protease.

98 (withdrawn): The method according to claim 97, wherein said protease is a member selected from the group consisting of aspartic protease, cysteine protease, metalloprotease and serine protease.

99 (withdrawn): A library of fluorogenic peptides comprising sub-libraries P1, P2, P3 and P4, wherein each of the sub-libraries P1, P2, P3 and P4 comprises hexapeptides having the structure:



wherein:

SS is a solid support, and

wherein:

for each sub-library P1, P2, P3 and P4, AA^1 , AA^2 , AA^3 and AA^4 in each of the hexapeptides are the same amino acid residues;

for sub-library P1, each of AA^5 is a different amino acid of the 20 amino acids, and each of AA^6 , AA^7 and AA^8 is an isokinetic mixture of 20 amino acids;

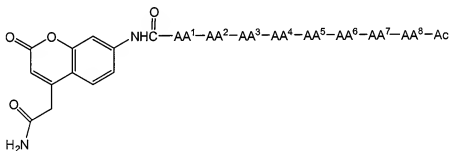
for sub-library P2, each of AA^6 is a different amino acid of the 20 amino acids, and each of AA^5 , AA^7 and AA^8 is an isokinetic mixture of 20 amino acids;

for sub-library P3, each of AA⁷ is a different amino acid of the 20 amino acids,
and each of AA⁵, AA⁶ and AA⁸ is an isokinetic mixture of 20 amino acids; and
for sub-library P4, each of AA⁸ is a different amino acid of the 20 amino acids,
and each of AA⁵, AA⁶ and AA⁷ is an isokinetic mixture of 20 amino acids.

100 (withdrawn): The library in accordance with claim 99, wherein the 20 amino acids are the 20 naturally occurring amino acids excluding cysteine and including norleucine.

101 (withdrawn): The library in accordance with claim 99, wherein the solid support is a Rink resin.

102 (withdrawn): A library of fluorogenic peptides comprising sub-libraries P1, P2, P3 and P4, wherein each of the sub-libraries P1, P2, P3 and P4 comprises hexapeptides having the structure:



wherein:

for each sub-library P1, P2, P3 and P4, AA¹, AA², AA³ and AA⁴ in each of the hexapeptides are the same amino acid residues;

for sub-library P1, each of AA⁵ is a different amino acid of the 20 amino acids,
and each of AA⁶, AA⁷ and AA⁸ is an isokinetic mixture of 20 amino acids;

for sub-library P2, each of AA⁶ is a different amino acid of the 20 amino acids,
and each of AA⁵, AA⁷ and AA⁸ is an isokinetic mixture of 20 amino acids;

for sub-library P3, each of AA⁷ is a different amino acid of the 20 amino acids,
and each of AA⁵, AA⁶ and AA⁸ is an isokinetic mixture of 20 amino acids; and
for sub-library P4, each of AA⁸ is a different amino acid of the 20 amino acids,
and each of AA⁵, AA⁶ and AA⁷ is an isokinetic mixture of 20 amino acids.

103 (withdrawn): The library in accordance with claim **102**, wherein the 20
amino acids are the 20 naturally occurring amino acids excluding cysteine and including
norleucine.

104 (withdrawn): A method of determining a peptide sequence specificity profile
of an enzymatically active protease, said method comprising:

(a) contacting said protease with a library of peptides according to claim **99** or
claim **102** in such a manner whereby the fluorogenic moiety is released
from the peptide sequence, thereby forming a fluorescent moiety;

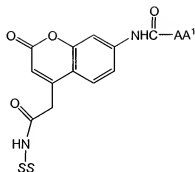
(b) detecting said fluorescent moiety;

(c) determining the sequence of said peptide sequence, thereby determining said
peptide sequence specificity profile of said protease.

105 (withdrawn): The method according to claim **104**, further comprising (d)
quantifying said fluorescent moiety, thereby quantifying said protease.

106 (withdrawn): The method according to claim **105**, wherein said protease is a
member selected from the group consisting of aspartic protease, cysteine protease,
metalloprotease and serine protease.

107 (withdrawn): A library of twenty fluorogenic amino acid amides having the
structure:



wherein:

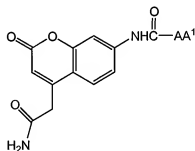
SS is a solid support, and

each AA¹ for the twenty fluorogenic amino acid amides is a different amino acid residue.

108 (withdrawn): The library in accordance with claim **107**, wherein the amino acid residues are the 20 naturally occurring amino acids excluding cysteine and including norleucine.

109 (withdrawn): The library in accordance with claim **108**, wherein the solid support is a Rink resin.

110 (withdrawn): A library of twenty fluorogenic amino acids having the structure:



wherein:

each AA¹ for the twenty fluorogenic amino acids is a different amino acid residue

1 **111** (withdrawn): The library in accordance with claim **110**, wherein the amino
2 acid residues are the 20 naturally occurring amino acids excluding cysteine and including
3 norleucine..

1 **112** (withdrawn): A method of determining an amino acid specificity profile of
2 an enzymatically active protease, said method comprising:

3 (a) contacting said protease with a library of amino acids according to claim **108**
4 or claim **110** in such a manner whereby the fluorogenic moiety is released
5 from the amino acid, thereby forming a fluorescent moiety;

6 (b) detecting said fluorescent moiety;

7 (c) determining the identity of the amino acid, thereby determining said amino
8 acid specificity profile of said protease.

1 **113** (withdrawn): The method according to claim **112**, further comprising (d)
2 quantifying said fluorescent moiety, thereby quantifying said protease.

1 **114** (withdrawn): The method according to claim **113**, wherein said protease is a
2 member selected from the group consisting of aspartic protease, cysteine protease,
3 metalloprotease and serine protease.